

RESULT 2

ABK92167

ID ABK92167 standard; DNA; 3810 BP.

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AC ABK92167;

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DT 15-AUG-2002 (first entry)

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DE

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KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.

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OS Mammalia.

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PN WO200230268-A2.

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PD 18-APR-2002.

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PF 12-OCT-2001; 2001WO-US032045.

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PR 13-OCT-2000; 2000US-00687576.

PR 08-DEC-2000; 2000US-00733288.

PR 08-DEC-2000; 2000US-00733742.

PR 24-JAN-2001; 2001US-0263957P.

PR 16-MAR-2001; 2001US-0276791P.

PR 16-MAR-2001; 2001US-0276888P.

PR 06-APR-2001; 2001US-0281922P.

PR 24-APR-2001; 2001US-0286214P.

PR 30-APR-2001; 2001US-00847046.

PR 04-MAY-2001; 2001US-0288589P.

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PA (EOSB-) EOS BIOTECHNOLOGY INC.

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PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;

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DR WPI; 2002-471335/50.

DR P-PSDB; ABG61852.

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PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.

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PS Claim 22; Page 339-340; 436pp; English.

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CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences

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SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3810
Score:	1123.00	Matches:	1123
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.6%	Indels:	0
DB:	6	Gaps:	0

US-10-643-795A-123 (1-1127) x ABK92167 (1-3810)

Qy 5 ThrGluLysProThrAspAlaTyrGlyGluLeuAspPheThrGlyAlaGlyArgLysHis 24

Db	3		ACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGCCGGCCGCAAGCAC	62
Qy	25		SerAsnPheLeuArgLeuSerAspArgThrAspProAlaAlaValTyrSerLeuValThr	44
Db	63		AGCAATTCCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTCACA	122
Qy	45		ArgThrTrpGlyPheArgAlaProAsnLeuValValSerValLeuGlyGlySerGlyGly	64
Db	123		CGCACATGGGGCTTCCGTGCCCCGAACCTGGTGGTGTACGTGCTGGGGGGATCGGGGGG	182
Qy	65		ProValLeuGlnThrTrpLeuGlnAspLeuLeuArgArgGlyLeuValArgAlaAlaGln	84
Db	183		CCCGTCCTCCAGACCTGGCTGCAGGACCTGCTGCGTCTGGGCTGGTGGGGCTGCCAG	242
Qy	85		SerThrGlyAlaTrpIleValThrGlyGlyLeuHisThrGlyIleGlyArgHisValGly	104
Db	243		AGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGCCGGCATGTTGGT	302
Qy	105		ValAlaValArgAspHisGlnMetAlaSerThrGlyGlyThrLysValValAlaMetGly	124
Db	303		GTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGACCAAGGTGGTGGCCATGGGT	362
Qy	125		ValAlaProTrpGlyValValArgAsnArgAspThrLeuIleAsnProLysGlySerPhe	144
Db	363		GTGGCCCCCTGGGGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGTTC	422
Qy	145		ProAlaArgTyrArgTrpArgGlyAspProGluAspGlyValGlnPheProLeuAspTyr	164
Db	423		CCTGCGAGGTACCGGTGGCGCGGTGACCCGAGGACGGGGTCCAGTTTCCCCTGGACTAC	482
Qy	165		AsnTyrSerAlaPhePheLeuValAspAspGlyThrHisGlyCysLeuGlyGlyGluAsn	184
Db	483		AACTACTCGGCCTTCTTCTGGTGGACGACGACACACGCTGCCTGGGGGCGGAGAAC	542
Qy	185		ArgPheArgLeuArgLeuGluSerTyrIleSerGlnGlnLysThrGlyValGlyGlyThr	204
Db	543		CGCTTCCGCTTGCGCCTGGAGTCTTACATCTCACAGCAGAAGACGGGCGTGGGAGGGACT	602
Qy	205		GlyIleAspIleProValLeuLeuLeuLeuIleAspGlyAspGluLysMetLeuThrArg	224
Db	603		GGAATTGACATCCCTGTCCTGCTCCTCTGATTGATGGTGTGAGAAGATGTTGACGCGA	662
Qy	225		IleGluAsnAlaThrGlnAlaGlnLeuProCysLeuLeuValAlaGlySerGlyGlyAla	244
Db	663		ATAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTCTCGTGGCTGGCTCAGGGGAGCT	722
Qy	245		AlaAspCysLeuAlaGluThrLeuGluAspThrLeuAlaProGlySerGlyGlyAlaArg	264
Db	723		GCGGACTGCCTGGCGGAGACCCTGGAAGACACTCTGGCCCCAGGGAGTGGGGGAGCCAGG	782
Qy	265		GlnGlyGluAlaArgAspArgIleArgArgPhePheProLysGlyAspLeuGluValLeu	284
Db	783		CAAGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGACCTTGAGGTCCTG	842
Qy	285		GlnAlaGlnValGluArgIleMetThrArgLysGluLeuLeuThrValTyrSerSerGlu	304
Db	843		CAGGCCAGGTGGAGAGGATTATGACCCGAAGGAGCTCCTGACAGTCTATTCTTCTGAG	902
Qy	305		AspGlySerGluGluPheGluThrIleValLeuLysAlaLeuValLysAlaCysGlySer	324
Db	903		GATGGGTCTGAGGAATTCGAGACCATAGTTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGC	962
Qy	325		SerGluAlaSerAlaTyrLeuAspGluLeuArgLeuAlaValAlaTrpAsnArgValAsp	344
Db	963		TCGGAGGCCTCAGCCTACCTGGATGAGCTGCGTTTGGCTGTGGCTTGAACCGCGTGGAC	1022
Qy	345		IleAlaGlnSerGluLeuPheArgGlyAspIleGlnTrpArgSerPheHisLeuGluAla	364
Db	1023		ATTGCCCAGAGTGAACCTTTTCGGGGGACATCCAATGGCGGTCTTCCATCTCGAAGCT	1082
Qy	365		SerLeuMetAspAlaLeuLeuAsnAspArgProGluPheValArgLeuLeuIleSerHis	384
Db	1083		TCCCTCATGGACGCCCTGCTGAATGACCGGCTGAGTTCGTGCGCTTGCTCATTTCCAC	1142
Qy	385		GlyLeuSerLeuGlyHisPheLeuThrProMetArgLeuAlaGlnLeuTyrSerAlaAla	404

Db	1143		GGCCTCAGCCTGGGCCACTTCCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCG	1202
Qy	405		ProSerAsnSerLeuIleArgAsnLeuLeuAspGlnAlaSerHisSerAlaGlyThrLys	424
Db	1203		CCCTCCAACCTCGCTCATCCGAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAA	1262
Qy	425		AlaProAlaLeuLysGlyGlyAlaAlaGluLeuArgProProAspValGlyHisValLeu	444
Db	1263		GCCCCAGCCCTAAAAGGGGAGCTGCGGAGCTCCGGCCCCCTGACGTGGGGCATGTGCTG	1322
Qy	445		ArgMetLeuLeuGlyLysMetCysAlaProArgTyrProSerGlyGlyAlaTrpAspPro	464
Db	1323		AGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCCTCCGGGGGCGCCTGGGACCCT	1382
Qy	465		HisProGlyGlnGlyPheGlyGluSerMetTyrLeuLeuSerAspLysAlaThrSerPro	484
Db	1383		CACCCAGGCCAGGGCTTCGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCG	1442
Qy	485		LeuSerLeuAspAlaGlyLeuGlyGlnAlaProTrpSerAspLeuLeuLeuTrpAlaLeu	504
Db	1443		CTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTG	1502
Qy	505		LeuLeuAsnArgAlaGlnMetAlaMetTyrPheTrpGluMetGlySerAsnAlaValSer	524
Db	1503		TTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAATGCAGTTTCC	1562
Qy	525		SerAlaLeuGlyAlaCysLeuLeuLeuArgValMetAlaArgLeuGluProAspAlaGlu	544
Db	1563		TCAGCTCTTGGGCGCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAG	1622
Qy	545		GluAlaAlaArgArgLysAspLeuAlaPheLysPheGluGlyMetGlyValAspLeuPhe	564
Db	1623		GAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTT	1682
Qy	565		GlyGluCysTyrArgSerSerGluValArgAlaAlaArgLeuLeuLeuArgArgCysPro	584
Db	1683		GGCGAGTGCTATCGCAGCAGTGAGGTGAGGGCTGCCCCGCTCCTCCTCCGTCGCTGCCCCG	1742
Qy	585		LeuTrpGlyAspAlaThrCysLeuGlnLeuAlaMetGlnAlaAspAlaArgAlaPhePhe	604
Db	1743		CTCTGGGGGGATGCCACTTGCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCTTCTTTT	1802
Qy	605		AlaGlnAspGlyValGlnSerLeuLeuThrGlnLysTrpTrpGlyAspMetAlaSerThr	624
Db	1803		GCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCACT	1862
Qy	625		ThrProIleTrpAlaLeuValLeuAlaPhePheCysProProLeuIleTyrThrArgLeu	644
Db	1863		ACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGGCCCTCCACTCATCTACCCCGCCTC	1922
Qy	645		IleThrPheArgLysSerGluGluGluProThrArgGluGluLeuGluPheAspMetAsp	664
Db	1923		ATCACCTTCAGGAAATCAGAAGAGAGCCACACGGGAGGAGCTAGAGTTTGACATGGAT	1982
Qy	665		SerValIleAsnGlyGluGlyProValGlyThrAlaAspProAlaGluLysThrProLeu	684
Db	1983		AGTGTCAATTAATGGGGAAGGCCTGTGCGGACGGCGGACCCAGCCGAGAAGACGCCGCTG	2042
Qy	685		GlyValProArgGlnSerGlyArgProGlyCysCysGlyGlyArgCysGlyGlyArgArg	704
Db	2043		GGGGTCCCGCGCCAGTCGGGCCCTCCGGGTGCTGCGGGGGCCGCTGCGGGGGGCGCCGG	2102
Qy	705		CysLeuArgArgTrpPheHisPheTrpGlyAlaProValThrIlePheMetGlyAsnVal	724
Db	2103		TGCCTACGCCGCTGGTTCCACTTCTGGGGCGCGCCGGTGACCATCTTCATGGGCAACGTG	2162
Qy	725		ValSerTyrLeuLeuPheLeuLeuLeuPheSerArgValLeuLeuValAspPheGlnPro	744
Db	2163		GTCAGCTACCTGCTGTCTTCTGCTGCTTTTCTCGCGGTGCTGCTCGTGGATTTCAGCCG	2222
Qy	745		AlaProProGlySerLeuGluLeuLeuLeuTyrPheTrpAlaPheThrLeuLeuCysGlu	764
Db	2223		GCGCCGCGCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAG	2282
Qy	765		GluLeuArgGlnGlyLeuSerGlyGlyGlyGlySerLeuAlaSerGlyGlyProGlyPro	784

Db	2283	GAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCGCCAGCGGGGCCCCGGGCCT	2342
Qy	785	GlyHisAlaSerLeuSerGlnArgLeuArgLeuTyrLeuAlaAspSerTrpAsnGlnCys	804
Db	2343	GGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAGTGC	2402
Qy	805	AspLeuValAlaLeuThrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeu	824
Db	2403	GACCTAGTGGCTCTCACCTGCTTCCTCCTGGGCGTGGGCTGCCGGCTGACCCGGGTTTG	2462
Qy	825	TyrHisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuLeu	844
Db	2463	TACCACCTGGGCGCACTGTCTCTGCATCGACTTCATGGTTTTTACGGTGCGGCTGCTT	2522
Qy	845	HisIlePheThrValAsnLysGlnLeuGlyProLysIleValIleValSerLysMetMet	864
Db	2523	CACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATG	2582
Qy	865	LysAspValPhePhePheLeuPhePheLeuGlyValTrpLeuValAlaTyrGlyValAla	884
Db	2583	AAGGACGTGTTCTTCTTCTTCTTCTTCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCC	2642
Qy	885	ThrGluGlyLeuLeuArgProArgAspSerAspPheProSerIleLeuArgArgValPhe	904
Db	2643	ACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCTCTTC	2702
Qy	905	TyrArgProTyrLeuGlnIlePheGlyGlnIleProGlnGluAspMetAspValAlaLeu	924
Db	2703	TACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCAGGAGGACATGGACGTGGCCCTC	2762
Qy	925	MetGluHisSerAsnCysSerSerGluProGlyPheTrpAlaHisProProGlyAlaGln	944
Db	2763	ATGGAGCACAGCAACTGCTCGTCGAGCCCGGCTTCTGGGCACACCCTCCTGGGGCCAG	2822
Qy	945	AlaGlyThrCysValSerGlnTyrAlaAsnTrpLeuValValLeuLeuLeuValIlePhe	964
Db	2823	GCGGGCACCTGCGTCTCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTC	2882
Qy	965	LeuLeuValAlaAsnIleLeuLeuValAsnLeuLeuIleAlaMetPheSerTyrThrPhe	984
Db	2883	CTGCTCGTGGCCAACATCCTGCTGCTCAACTTGCTCATTGCCATGTTAGTTACACATTC	2942
Qy	985	GlyLysValGlnGlyAsnSerAspLeuTyrTrpLysAlaGlnArgTyrArgLeuIleArg	1004
Db	2943	GGCAAAGTACAGGGCAACAGCATCTCTACTGGAAGCGCAGCGTTACCGCCTCATCCGG	3002
Qy	1005	GluPheHisSerArgProAlaLeuAlaProProPheIleValIleSerHisLeuArgLeu	1024
Db	3003	GAATTCCTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTC	3062
Qy	1025	LeuLeuArgGlnLeuCysArgArgProArgSerProGlnProSerSerProAlaLeuGlu	1044
Db	3063	CTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCAGCCGTCTCCCGGCCCTCGAG	3122
Qy	1045	HisPheArgValTyrLeuSerLysGluAlaGluArgLysLeuLeuThrTrpGluSerVal	1064
Db	3123	CATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTG	3182
Qy	1065	HisLysGluAsnPheLeuLeuAlaArgAlaArgAspLysArgGluSerAspSerGluArg	1084
Db	3183	CATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGT	3242
Qy	1085	LeuGluArgThrSerGlnLysValAspLeuAlaLeuLysGlnLeuGlyHisIleArgGlu	1104
Db	3243	CTGGAGCGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAG	3302
Qy	1105	TyrGluGlnArgLeuLysValLeuGluArgGluValGlnGlnCysSerArgValLeuGly	1124
Db	3303	TACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCTGGGG	3362
Qy	1125	TrpValThr	1127
Db	3363	TGGGTGACG	3371

